

#5

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/511,538

Source: PCT/10

Date Processed by STIC: 10/27/04

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 10/27/2004

PATENT APPLICATION: US/10/511,538

TIME: 10:51:43

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\10272004\J511538.raw

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3 <110> APPLICANT: OriGene Technologies, Inc
5 <120> TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
7 <130> FILE REFERENCE: 16U 200 PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/511,538
C--> 9 <141> CURRENT FILING DATE: 2004-10-18
9 <150> PRIOR APPLICATION NUMBER: US 60/372,669
10 <151> PRIOR FILING DATE: 2002-04-16
12 <150> PRIOR APPLICATION NUMBER: US 60/411,882
13 <151> PRIOR FILING DATE: 2002-09-20
15 <150> PRIOR APPLICATION NUMBER: US 60/424,336
16 <151> PRIOR FILING DATE: 2002-11-07
18 <150> PRIOR APPLICATION NUMBER: US 60/374,823
19 <151> PRIOR FILING DATE: 2002-04-24
21 <150> PRIOR APPLICATION NUMBER: US 60/376,558
22 <151> PRIOR FILING DATE: 2002-05-01
24 <150> PRIOR APPLICATION NUMBER: US 60/381,366
25 <151> PRIOR FILING DATE: 2002-05-20
27 <150> PRIOR APPLICATION NUMBER: US 60/403,648
28 <151> PRIOR FILING DATE: 2002-08-16
30 <160> NUMBER OF SEQ ID NOS: 344
32 <170> SOFTWARE: PatentIn version 3.1
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35 <211> LENGTH: 795
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
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40 <221> NAME/KEY: CDS
41 <222> LOCATION: (1)..(795)
42 <223> OTHER INFORMATION:
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46 Met Glu Arg Val Asn Glu Thr Val Val Arg Glu Val Ile Phe Leu Gly
47 1          5          10          15
49 ttc tca tcc ctg gcc agg ctg cag cag ctg ctc ttt gtt atc ttc ctg      96
50 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu
51          20          25          30
53 ctc ctc tac ctg ttc act ctg gcc acc aat gca atc atc att tcc acc      144
54 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr
55          35          40          45
57 att gtc ctg gac agg gcc ctt cat atc ccc atg tac ttc ttc ctt gcc      192
58 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala
59          50          55          60
61 atc ctc tct tgc tct gag att tgc tac acc ttc atc att gta ccc aag      240

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62 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Ile Ile Val Pro Lys
63 65 70 75 80
65 atg ctg gtt gac ctg ctg tcc cag aag aag acc att tct ttc ctg ggc 288
66 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly
67 85 90 95
69 tgt gcc atc caa atg ttt tcc ttc ctc ttc ctt ggc tgc tct cac tcc 336
70 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Leu Gly Cys Ser His Ser
71 100 105 110
73 ttt ctg ctg gca gtc atg ggt tat gat cgt tac ata gcc atc tgt aac 384
74 Phe Leu Leu Ala Val Met Gly Tyr Asp Arg Tyr Ile Ala Ile Cys Asn
75 115 120 125
77 cca ctg cgc tac tca gtg cta atg gga cat ggg gtg tgt atg gga cta 432
78 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu
79 130 135 140
81 gtg gct gct gcc tgt gcc tgt ggc ttc act gtt gca cag atc atc aca 480
82 Val Ala Ala Ala Cys Ala Cys Gly Phe Thr Val Ala Gln Ile Ile Thr
83 145 150 155 160
85 tcc ttg gta ttt cac ctg cct ttt tat tcc tcc aat caa cta cat cac 528
86 Ser Leu Val Phe His Leu Pro Phe Tyr Ser Ser Asn Gln Leu His His
87 165 170 175
89 ttc ttc tgt gac att gct cct gtc ctc aag ctg gca tct cac cat aac 576
90 Phe Phe Cys Asp Ile Ala Pro Val Leu Lys Leu Ala Ser His His Asn
91 180 185 190
93 cac ttt agt cag att gtc atc ttc atg ctc tgt aca ttg gtc ctg gct 624
94 His Phe Ser Gln Ile Val Ile Phe Met Leu Cys Thr Leu Val Leu Ala
95 195 200 205
97 atc ccc tta ttg ttg atc ttg gtg tcc tat gtt cac atc ctc tct gcc 672
98 Ile Pro Leu Leu Leu Ile Leu Val Ser Tyr Val His Ile Leu Ser Ala
99 210 215 220
101 ata ctt cag ttt cct tcc aca ctg gga gtg ata gca aaa agg aag ttt 720
102 Ile Leu Gln Phe Pro Ser Thr Leu Gly Val Ile Ala Lys Arg Lys Phe
103 225 230 235 240
105 cac aat agt gat gat ttc tca cat tat aac tct ttt caa gat cca cct 768
106 His Asn Ser Asp Asp Phe Ser His Tyr Asn Ser Phe Gln Asp Pro Pro
107 245 250 255
109 gtc aat aaa agt ctc ctg att gat taa 795
110 Val Asn Lys Ser Leu Leu Ile Asp
111 260
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115 <211> LENGTH: 264
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
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122 1 5 10 15
125 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu
126 20 25 30
129 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr
130 35 40 45

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133 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala
134      50                      55                      60
137 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Ile Ile Val Pro Lys
138 65                      70                      75                      80
141 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly
142                      85                      90                      95
145 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Leu Gly Cys Ser His Ser
146                      100                      105                      110
149 Phe Leu Leu Ala Val Met Gly Tyr Asp Arg Tyr Ile Ala Ile Cys Asn
150                      115                      120                      125
153 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu
154                      130                      135                      140
157 Val Ala Ala Ala Cys Ala Cys Gly Phe Thr Val Ala Gln Ile Ile Thr
158 145                      150                      155                      160
161 Ser Leu Val Phe His Leu Pro Phe Tyr Ser Ser Asn Gln Leu His His
162                      165                      170                      175
165 Phe Phe Cys Asp Ile Ala Pro Val Leu Lys Leu Ala Ser His His Asn
166                      180                      185                      190
169 His Phe Ser Gln Ile Val Ile Phe Met Leu Cys Thr Leu Val Leu Ala
170                      195                      200                      205
173 Ile Pro Leu Leu Leu Ile Leu Val Ser Tyr Val His Ile Leu Ser Ala
174                      210                      215                      220
177 Ile Leu Gln Phe Pro Ser Thr Leu Gly Val Ile Ala Lys Arg Lys Phe
178 225                      230                      235                      240
181 His Asn Ser Asp Asp Phe Ser His Tyr Asn Ser Phe Gln Asp Pro Pro
182                      245                      250                      255
185 Val Asn Lys Ser Leu Leu Ile Asp
186                      260
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190 <211> LENGTH: 32
191 <212> TYPE: DNA
192 <213> ORGANISM: Homo sapiens
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199 <211> LENGTH: 31
200 <212> TYPE: DNA
201 <213> ORGANISM: Homo sapiens
203 <400> SEQUENCE: 4
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208 <211> LENGTH: 50
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo sapiens
212 <400> SEQUENCE: 5
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216 <210> SEQ ID NO: 6
217 <211> LENGTH: 807
218 <212> TYPE: DNA

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219 <213> ORGANISM: Homo sapiens
 221 <220> FEATURE:
 222 <221> NAME/KEY: CDS
 223 <222> LOCATION: (1)..(807)
 224 <223> OTHER INFORMATION:
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 227 atg gcc gtt att cgc ttc agc tgg act ctc cac act ccc atg tat ggc 48
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 229 1 5 10 15
 231 ttt cta ttc atc ctt tca ttt tct gag tcc tgc tac act ttt gtc atc 96
 232 Phe Leu Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile
 233 20 25 30
 235 atc cct cag ctg ctg gtc cac ctg ctc tca gac acc aag acc atc tcc 144
 236 Ile Pro Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser
 237 35 40 45
 239 ttc atg gcc tgt gcc acc cag ctg ttc ttt ttc ctt ggc ttt gct tgc 192
 240 Phe Met Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys
 241 50 55 60
 243 acc aac tgc ctc ctc att gct gtg atg gga tat gat cgc tat gta gca 240
 244 Thr Asn Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala
 245 65 70 75 80
 247 att tgt cac cct ctg agg tac aca ctc atc ata aac aaa agg ctg ggg 288
 248 Ile Cys His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly
 249 85 90 95
 251 ttg gag ttg att tct ctc tca gga gcc aca ggt ttc ttt att gct ttg 336
 252 Leu Glu Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu
 253 100 105 110
 255 gtg gcc acc aac ctc att tgt gac atg cgt ttt tgt ggc ccc aac agg 384
 256 Val Ala Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg
 257 115 120 125
 259 gtt aac cac tat ttc tgt gac atg gca cct gtt atc aag tta gcc tgc 432
 260 Val Asn His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys
 261 130 135 140
 263 act gac acc cat gtg aaa gag ctg gct tta ttt agc ctc agc atc ctg 480
 264 Thr Asp Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu
 265 145 150 155 160
 267 gta att atg gtg cct ttt ctg tta att ctc ata tcc tat ggc ttc ata 528
 268 Val Ile Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile
 269 165 170 175
 271 gtt aac acc atc ctg aag atc ccc tca gct gag ggc aag aag gcc ttt 576
 272 Val Asn Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe
 273 180 185 190
 275 gtc acc tgt gcc tca cat ctc act gtg gtc ttt gtc cac tat ggc tgt 624
 276 Val Thr Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys
 277 195 200 205
 279 gcc tct atc atc tat ctg cgg ccc aag tcc aag tct gcc tca gac aag 672
 280 Ala Ser Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys
 281 210 215 220
 283 gat cag ttg gtg gca gtg acc tac aca gtg gtt act ccc tta ctt aat 720

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284 Asp Gln Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn
285 225                230                235                240
287 cct ctt gtc tac agt ctg agg aac aaa gag gta aaa act gca ttg aaa      768
288 Pro Leu Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys
289                245                250                255
291 aga gtt ctt gga atg cct gtg gca acc aag atg agc taa      807
292 Arg Val Leu Gly Met Pro Val Ala Thr Lys Met Ser
293                260                265
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 268
298 <212> TYPE: PRT
299 <213> ORGANISM: Homo sapiens
301 <400> SEQUENCE: 7
303 Met Ala Val Ile Arg Phe Ser Trp Thr Leu His Thr Pro Met Tyr Gly
304 1                5                10                15
307 Phe Leu Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile
308                20                25                30
311 Ile Pro Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser
312                35                40                45
315 Phe Met Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys
316 50                55                60
319 Thr Asn Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala
320 65                70                75                80
323 Ile Cys His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly
324                85                90                95
327 Leu Glu Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu
328                100               105               110
331 Val Ala Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg
332                115               120               125
335 Val Asn His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys
336 130               135               140
339 Thr Asp Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu
340 145               150               155               160
343 Val Ile Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile
344                165               170               175
347 Val Asn Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe
348                180               185               190
351 Val Thr Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys
352                195               200               205
355 Ala Ser Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys
356 210               215               220
359 Asp Gln Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn
360 225               230               235               240
363 Pro Leu Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys
364                245               250               255
367 Arg Val Leu Gly Met Pro Val Ala Thr Lys Met Ser
368                260               265
371 <210> SEQ ID NO: 8
372 <211> LENGTH: 25

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/511,538

DATE: 10/27/2004

TIME: 10:51:44

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\10272004\J511538.raw

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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